

CD105PCT ST25 (2).txt
SEQUENCE LISTING

<110> CropDesign N.V.

<120> Seedy1 sequence for making plants having changed growth characteristics

<130> CD-105-PCT

<150> US 60/528,113
<151> 2003-12-09

<150> EP 03104280.7
<151> 2003-11-19

<160> 18

<170> PatentIn version 3.3

<210> 1
<211> 1428
<212> DNA
<213> Nicotiana tabacum

<220>
<221> misc_feature
<223> seedy1 coding sequence (CDS0689)

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ctgaaacccc tttcggtttag gccatcagat tcctttgaat ctgatttgtc aagtaaggaa 180
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aaacagagtc ttgatgagat ggcggctaga aagagcggaa agggaaatga tttccgtgat 360
gagaagaaaa tagacgagga aattgaagaa attcagatgg agattagtag gttgagttca 420
agattagagg ctttgagaat tgaaaaggct gagaaaactg ttgctaagac tgttgaaaag 480
cgaggaaggg ttgtggcagc aaagtttatg gagccaaaac aaagtgttat taagattgaa 540
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ccatctgaga tttttactgg aacgcggcgg cgagggttga gtatggggcc atcagatatt 660
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ttgagttcag ttcagccaaa gaagttgttt aaagatctcg aaaagtctgc tgctgctaata 960
aagaagcccc agaggccggg gagggttgtg gctagtaggt ataatacagag tacaattcag 1020

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tcatacagtag tgagaaagag gtctttacct gaaaatgata aggatgagag taagagaaat 1080
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<210> 2
<211> 475
<212> PRT
<213> Nicotiana tabacum

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<220>
<221> MISC_FEATURE
<223> seedy1 protein (CDS0689)

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<400> 2

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Met Ser Val Leu Gln Tyr Pro Glu Gly Ile Asp Pro Ala Asp Val Gln
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Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Leu Ser
          20          25          30

```

```

Ser Leu Lys Arg Ser Trp Ser Pro Leu Lys Pro Leu Ser Val Arg Pro
          35          40          45

```

```

Ser Asp Ser Phe Glu Ser Asp Leu Ser Ser Lys Glu Asn Gln Thr Pro
          50          55          60

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```

Leu Phe Glu Asn Ser Ser Val Asn Leu Ser Ser Pro Leu Pro Ile Lys
          65          70          75          80

```

```

Pro Leu Asn Pro Asn Gly Ala Leu Glu Asn Ser Arg Leu Lys Pro Asn
          85          90          95

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```

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser
          100          105          110

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Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile
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Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala
          130          135          140

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Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys
 145 150 155 160
 Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val
 165 170 175
 Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu
 180 185 190
 Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr
 195 200 205
 Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr
 210 215 220
 Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile
 225 230 235 240
 Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu
 245 250 255
 Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys
 260 265 270
 Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile
 275 280 285
 Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val
 290 295 300
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 305 310 315 320
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 325 330 335
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 340 345 350
 Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val
 355 360 365
 Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu
 370 375 380
 Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His
 385 390 395 400

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Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro
405 410 415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu
420 425 430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys
435 440 445

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Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu
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<211> 1336
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<223> seedy1 coding sequence

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gccgagatcg gccacatcga ggcggagatc ctgcgcctct cgtcccggct ccaccatctc 240
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aaggtgaggc cccggccgag gggcctcagc ctcgggcccc tggatgtgat ctccatcgtc 360
aatcgtgaga agcatccgct gcgcaccaag cagcctccgg cgacgcgggg cagggggctc 420
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cagcaacagc aacgcgctgg cacggcgcgg atcctgaagc caatcaagga gcctccggtg 540
cagcgtcgca ggggcgtcag cctcgggccg ttggagatcc accacggcgt cggcagcaag 600
gcaccagcgg cggcgcgagc caagccgttc accaccaagc tcaacgccat tcgagaagaa 660
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cccaggccca ggaggcaatc caatggcaag gctactgaca caaggggagg caacaagggtg 840
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<210> 4
<211> 431
<212> PRT
<213> Oryza sativa

<220>
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<223> seedy1 protein
<400> 4

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20 25 30
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35 40 45
Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly
50 55 60
His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu
65 70 75 80
Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly
85 90 95
Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly
100 105 110
Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg
115 120 125
Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro
130 135 140

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Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His
145 150 155 160

Gln Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys
165 170 175

Glu Pro Pro Val Gln Arg Arg Arg Gly Val Ser Leu Gly Pro Leu Glu
180 185 190

Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys
195 200 205

Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser
210 215 220

Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg
225 230 235 240

Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala
245 250 255

Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr
260 265 270

Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly
275 280 285

Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Ala Thr Ala Lys
290 295 300

Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser
305 310 315 320

Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg
325 330 335

Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu
340 345 350

Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro
355 360 365

Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met
370 375 380

Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val

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395

385 390 400

Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp
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Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala
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<210> 5
<211> 1860
<212> DNA
<213> Medicago trunculata

<220>
<221> misc_feature
<223> seedy1 coding sequence

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tttattttctt cctctttcaa tctccaacgg tcacataatc tcttccaaat acaaataatt 240
ccctctttca acctcactct tcatttcttc aacccaaacc caaaaaacta atcagattct 300
tcttaaattct tgaaaccttt ctcccaaag cacttaaata aaaaagcact taaccatgaa 360
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tttcaaggag gagacaccga aacgaaacgg tgctgtttcg gatacgccga aatctagggt 780
taattggaga agagggatga gtttaggtcc gatggagatt gccgggaaag tgatggcacc 840
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gcaggaaagt tgtgaagtaa tgccgtcggg gattactccg gcgacggtga ataggaggaa 960
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gaagaagaaa gatgaagaaa ttgctcaggt tcaaccgaag aagctgtttg aaggtgaaaa 1140
atcagtgaag aaatcgttga aacaaggtag aattgttgca agccggtata attccggtgg 1200
tggtggtggt gatgagagga aaagatcggt ttcggagaat aataagggtt tagggagtga 1260

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 agatgatgat gatgatgatg attatgggtga acaagggtaa ttgtggaaat tggaattgat 1560
 ttgtttttgt ggggtttgtg ggaactggct atgttctgct tgattctttt gcattttggt 1620
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<210> 6
 <211> 394
 <212> PRT
 <213> Medicago trunculata

<220>
 <221> MISC_FEATURE
 <223> seedy1 protein
 <400> 6

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 Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn
 35 40 45
 Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu
 50 55 60
 Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg
 65 70 75 80
 Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly
 85 90 95
 Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys
 100 105 110
 Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro
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115

120

125

Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp
130 135 140

Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met
145 150 155 160

Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys
165 170 175

Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly
180 185 190

Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro
195 200 205

Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn
210 215 220

Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys
225 230 235 240

Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys
245 250 255

Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg
260 265 270

Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Gly Asp Ala Arg
275 280 285

Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg
290 295 300

Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly
305 310 315 320

Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser
325 330 335

Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys
340 345 350

Arg Ser Tyr Phe Cys Asp Glu Asp Glu Glu Glu Arg Val Met Val Glu
355 360 365

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Glu Glu Gly Gly Ser Val Cys Gln Val Leu Asn Phe Ala Glu Asp Asp
 370 375 380

Asp Asp Asp Asp Asp Tyr Gly Glu Gln Gly
 385 390

<210> 7
 <211> 674
 <212> DNA
 <213> Saccharum sp.

<220>
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 <223> seedy1 coding sequence (partial 5' end)

<220>
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 <222> (362)..(362)
 <223> n can be a, c, g or t

<220>
 <221> misc_feature
 <222> (372)..(372)
 <223> n can be a, c, g or t

<220>
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 <222> (674)..(674)
 <223> n can be a, c, g or t

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 tccgggtccag ggggctctcc ggcggcggtg gcgatggagg aggacccgct catcccgtg 180
 gtgcacgtct ggaacaacgc cgccttcgac cagcctcct cctccgcgtg gcacgcccac 240
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 gacaaccagc agcagcagcc gcgtgccgcg cagggtctga agccgatcaa gcaggccacg 600
 gcggcgggcg gcaagggcgt aagacttggg ccccttcgac atggtcggcg cgaaccctag 660
 ggtccctccg ccn 674

<210> 8
 <211> 166
 <212> PRT
 <213> Saccharum sp.

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<220>
<221> MISC_FEATURE
<223> seedy1 protein

<220>
<221> MISC_FEATURE
<223> seedy1 protein (partial N term)

<220>
<221> MISC_FEATURE
<222> (70)..(70)
<223> Xaa can be any amino acid

<400> 8

Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala
1 5 10 15

Ala Phe Asp His Ala Ser Ser Ser Ala Trp His Ala His Ser Pro Val
20 25 30

Pro Ala Ser Ala Arg Arg Glu Ala Glu Gly Asp Lys Glu Asn His Arg
35 40 45

Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala
50 55 60

Glu Ile Leu Arg Leu Xaa Ser Arg Leu His His Leu Arg Thr Ser Lys
65 70 75 80

Gln Ser Glu Pro Ser Lys Arg Gly Glu Val Ala Pro Ala Pro Ala Ala
85 90 95

Lys Ala Lys Ala Ala Ala Ala Arg Leu Arg Thr Arg Gly Leu Ser
100 105 110

Leu Gly Pro Leu Asp Val Ala Ala Ala Gly Asn Pro Asn Pro Leu Thr
115 120 125

Thr Asp Asn Gln Gln Gln Gln Pro Arg Ala Ala Gln Gly Leu Lys Pro
130 135 140

Ile Lys Gln Ala Thr Ala Ala Ala Gly Lys Gly Val Arg Leu Gly Pro
145 150 155 160

Leu Arg His Gly Arg Arg
165

<210> 9
<211> 876

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<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<223> seedy1 coding sequence (partial 3' end)

<220>
<221> misc_feature
<222> (869)..(869)
<223> n = a, c, g or t

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caagcagagc caaggcgagg agcgggagca taagccccag caggttcagg aggcagtcca      180
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<210> 10
<211> 224
<212> PRT
<213> Zea mays

<220>
<221> MISC_FEATURE
<223> seedy1 protein (partial C term)

<400> 10

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1 5 10 15

Ala Val Pro Ala Arg Pro Trp Pro Ser Ser Asn Ala Arg His Pro Leu
20 25 30

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Asp Ala Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala Arg Ser Gly
35 40 45

Ser Ile Ser Pro Ser Arg Phe Arg Arg Gln Ser Thr Ser Lys Ala Ala
50 55 60

Glu Thr Arg Ala Gly Asn Ala Lys Pro Thr Glu Ala Thr Arg Gly Gly
65 70 75 80

Ser Glu Ala Val Asn His Thr Ser Asn Val Ala Thr Thr Lys Arg Pro
85 90 95

Ala Gly Ser Ser Lys Val Arg Val Val Pro Ser Arg Tyr Ser Ile Pro
100 105 110

Pro Gly Ser Ser Leu Ala Ala Val Thr Gln Gly Asn Arg Cys Lys Gln
115 120 125

Ser Leu Pro Gly Ser Ala Thr Glu Thr Arg Val Asn Leu Thr Glu Pro
130 135 140

Pro Asn Asp Glu Leu Ser Pro Glu Glu Leu Ala Lys Val Ala Glu Leu
145 150 155 160

Leu Pro Arg Ile Arg Thr Met Pro Pro Ser Asp Glu Ser Pro Arg Asp
165 170 175

Ser Gly Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe
180 185 190

Phe Thr Ala Ala Gly Asp Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala
195 200 205

Arg Val Val Glu Leu Glu Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu
210 215 220

<210> 11
<211> 1257
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<223> seedy1 coding sequence

<400> 11
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CD105PCT.ST25 (2).txt

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gaagaagtag agaaggagat cggacgatta tcgacgaaat tggagtcgct ccgattagag 360
aaggcggagc aaaccgcaag aagcattgct atacgtggaa gaatcgttcc ggcgaagttc 420
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 35 40 45

CD105PCT ST25 (2).txt

Ser Asp Cys Ser Lys Glu Asn Gln Phe Pro Ile Ser Val Ser Ser Ser
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Leu Gln Ser Ser Val Ser Ile Thr Glu Ala Pro Ser Ala Lys Ser Lys
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Thr Val Lys Thr Lys Ser Ala Ala Asp Arg Ser Lys Lys Arg Asp Ile
85 90 95

Asp Ala Glu Ile Glu Glu Val Glu Lys Glu Ile Gly Arg Leu Ser Thr
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Lys Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Thr Ala Arg Ser
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Ile Ala Ile Arg Gly Arg Ile Val Pro Ala Lys Phe Met Glu Ser Ser
130 135 140

Gln Lys Gln Val Lys Phe Asp Asp Ser Cys Phe Thr Gly Ser Lys Ser
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Arg Ala Thr Arg Arg Gly Val Ser Leu Gly Pro Ala Glu Ile Phe Asn
165 170 175

Ser Ala Lys Lys Ser Glu Thr Val Thr Pro Leu Gln Ser Ala Gln Asn
180 185 190

Arg Arg Lys Ser Cys Phe Phe Lys Leu Pro Gly Ile Glu Glu Gly Gln
195 200 205

Val Thr Thr Arg Gly Lys Gly Arg Thr Ser Leu Ser Leu Ser Pro Arg
210 215 220

Ser Arg Lys Ala Lys Met Thr Ala Ala Gln Lys Gln Ala Ala Thr Thr
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Val Gly Ser Lys Arg Ala Val Lys Lys Glu Glu Gly Val Leu Leu Thr
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Ile Gln Pro Lys Arg Leu Phe Lys Glu Asp Glu Lys Asn Val Ser Leu
260 265 270

Arg Lys Pro Leu Lys Pro Gly Arg Val Val Ala Ser Arg Tyr Ser Gln
275 280 285

Met Gly Lys Thr Gln Thr Gly Glu Lys Asp Val Arg Lys Arg Ser Leu
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295

Pro Glu Asp Glu Glu Lys Glu Asn His Lys Arg Ser Glu Lys Arg Arg
305 310 315 320

Ala Ser Asp Glu Ser Asn Lys Ser Glu Gly Arg Val Lys Lys Arg Trp
325 330 335

Glu Ile Pro Ser Glu Val Asp Leu Tyr Ser Ser Gly Glu Asn Gly Asp
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Glu Ser Pro Ile Val Lys Glu Leu Pro Lys Ile Arg Thr Leu Arg Arg
355 360 365

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CD105PCT ST25 (2).txt

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CD105PCT ST25 (2).txt

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CD105PCT ST25 (2).txt

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 <223> Motif 3 (coiled coil) CORE SEQUENCE

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CD105PCT ST25 (2).txt

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